

In the Drawings:

Please replace FIG. 2-1 to 2-8 with replacement drawings FIG. 2-1 to 2-8.

REMARKS

Claims 1-28 and 30-43 were pending prior to entering the amendments.

The Amendments

The Table at pages 43 and 44 is amended to insert SEQ ID NOs.

At page 45, an obvious typographic error of “figure 5” is amended to “figure 2;” there is no figure 5 in the application and the text refers to the frameshift peptide of Figure 2.

Claims 1-43 are cancelled. New Claims 44-79 are added.

Claim 44 is supported by FIG. 2-1 and 2-2.

Claim 45 is supported by original Claim 3(d), page 8, lines 27-29, page 10, line 27 to page 11, line 5.

Claim 46 is supported by page 11, lines 8-11.

Claim 47 is supported by FIG. 2-2, TAF1b (-1).

Claim 48 is supported by FIG. 2-2, TAF1b (+1).

Claim 49 is supported by FIG. 2-1, HT001 (-1).

Claim 50 is supported by FIG. 2-1, HT001 (+1).

Claims 51-56 are supported by page 22, lines 17-18.

Claims 57-62 are supported by page 34, lines 11-16.

Claim 63 is supported by original Claims 18, 24, and 30, FIG. 2-1, FIG. 2-2, page 22, lines 17-18.

Claim 64 is supported by original Claim 3(d), page 8, lines 27-29, page 10, line 27 to page 11, line 5.

Claim 65 is supported by page 11, lines 8-11.

Claim 66 is supported by FIG. 2-2, TAF1b (-1).

Claim 67 is supported by FIG. 2-2, TAF1b (+1).

Claim 68 is supported by FIG. 2-1, HT001 (-1).

Claim 69 is supported by FIG. 2-1, HT001 (+1).

Claim 70 is supported by FIG. 2-1, TGFbRII (-1).

Claim 71 is supported by FIG. 2-1, TGFbRII (+1).

Claim 72 is supported by original Claims 18, 24, and 30; FIGs. 2-1 and 2-2; and page 34, lines 11-16.

Claim 73 is supported by original Claim 3(d), page 8, lines 27-29, page 10, line 27 to page 11, line 5.

Claim 74 is supported by FIG. 2-2, TAF1b (-1).

Claim 75 is supported by FIG. 2-2, TAF1b (+1).

Claim 76 is supported by FIG. 2-1, HT001 (-1).

Claim 77 is supported by FIG. 2-1, HT001 (+1).

Claim 78 is supported by FIG. 2-1, TGFbRII (-1).

Claim 79 is supported by FIG. 2-1, TGFbRII (+1).

The amendments in the drawings (FIGs. 2-1 to 2-8) are to insert sequence ID numbers. A marked copy of the drawings which shows the changes are included.

No new matter is added in any of the amendment. The Examiner is requested to enter the amendments.

Election/Restriction

Claims 3, 4, 11, 17, 30 and 31 were examined.

New Claims 40-50 correspond to the invention of Claim 3. New Claims 51-56 correspond to the invention of Claim 11. New claims 57-62 correspond to the invention of Claim 17. New Claims 63-69 correspond to the invention of Claim 30 (a).

New Claim 70-79 correspond to the elected invention, i.e., the combination of at least three polypeptides HT001, GGFBR2, and TAF1B (see Restriction Requirement at page 4, Group I, dated January 11, 2008, and Response to Restriction Requirement dated July 9, 2008).

The Response

35 U.S.C. §101 Rejection

Claims 3 and 4 are rejected under 35 U.S.C. 101. Claims 3-4 are cancelled.

New Claim 44 recites an isolated frameshift polypeptide. Therefore, the §101 Rejection should be withdrawn.

Claim Objections

Claims 4 and 31 are objected to under 37 CFR 1.75(c), as being of improper dependent form. Claims 4 and 31 are cancelled.

35 U.S.C. § 112, First Paragraph, Rejection – Written Description

Claims 3, 4, 11, 17, 30, and 31 are rejected under 35 U.S.C. 112, first paragraph, as allegedly failing to comply with the written description requirement for the following reasons:

Claims 3, 4, 11, 17, 30, and 31 are cancelled.

New Claims 44-79 are directed to frameshift polypeptide TAF1b (-1) ORF, TAF1b (+1) ORF, TAF1b (-2) ORF, HT001 (-1) ORF, HT001 (+1) ORF, HT001 (-2) ORF, TGFbRII (-1) ORF, TGFbRII (+1) ORF, and TGFbRII (-2). Each of the sequences is identified in FIGs. 2-1 and 2-2.

Therefore, the written description rejection should be withdrawn.

35 U.S.C. § 102(b) Rejection

Claims 3, 4, 11, 17, 30, and 31 are rejected under 35 U.S.C. 102(b) as being anticipated by Yang et al (Molecular and Cellular Biology, November 1996, 16(11):6603-6616). The rejection is traversed.

Yang et al. disclose that GCN3, GCD7 and GCD2 are regulatory domains in the guanine nucleotide exchange factor eIF2B. These proteins do not have any relationship to the subject matter of the present application. Furthermore, Yang et al. do not disclose the amino acid sequences of the claimed frameshift polypeptides of SEQ ID Nos: 2, 3, 20, 21, and 117-120.

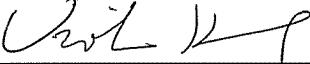
Therefore, the 102(b) rejection should be withdrawn.

CONCLUSION

Applicants believe that the application is now in good and proper condition for allowance.
Early notification of allowance is earnestly solicited.

Respectfully submitted,

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Enclosures: Replacement Drawings and Marked-Up Drawings

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FIG. 2-1**HT001****wt ORF (SEQ ID NO: 1)**

MQRPNNAHRISQPIRQIYGLLLNASPHLDKTSWNALPPQPLAFSEVERINKNIRTSIIDAVELAKDHSDLSRLTELSRRRQMLLETLKV
KQTILEPIPTSLKLPiAVSCYWLQHETKAKLHHLQSLLTMLVGLPIAIINSPGKEELQEDGAKMLYAEFQRVKAQTRLGTRLDLDTAHI
FCQWQSCLQMGMLNQLLSTPLPEPDLTLYSGSLVHGLCQQLLASTSVESLLSICPEAKQLYEYLNFATRSYAPAEIFLPKGRSN SK
KKRQKKQNTCSKNRGRRTAHTKWCWYEGNNRFGLMVENLEEHSEASNIE

(-1) ORF (SEQ ID NO: 2)

MQRPNNAHRISQPIRQIYGLLLNASPHLDKTSWNALPPQPLAFSEVERINKNIRTSIIDAVELAKDHSDLSRLTELSRRRQMLLETLKV
KQTILEPIPTSLKLPiAVSCYWLQHETKAKLHHLQSLLTMLVGLPIAIINSPGKEELQEDGAKMLYAEFQRVKAQTRLGTRLDLDTAHI
FCQWQSCLQMGMLNQLLSTPLPEPDLTLYSGSLVHGLCQQLLASTSVESLLSICPEAKQLYEYLNFATRSYAPAEIFLPKGRSN SK
KKGRRNRPRAVLTEGEPLHTPSVGMRETTGLGC

(+1)(-2) ORF (SEQ ID NO: 3/118)

MQRPNNAHRISQPIRQIYGLLLNASPHLDKTSWNALPPQPLAFSEVERINKNIRTSIIDAVELAKDHSDLSRLTELSRRRQMLLETLKV
KQTILEPIPTSLKLPiAVSCYWLQHETKAKLHHLQSLLTMLVGLPIAIINSPGKEELQEDGAKMLYAEFQRVKAQTRLGTRLDLDTAHI
FCQWQSCLQMGMLNQLLSTPLPEPDLTLYSGSLVHGLCQQLLASTSVESLLSICPEAKQLYEYLNFATRSYAPAEIFLPKGRSN SK
KK(K)AEETEYQLF

U79260**wt ORF (SEQ ID NO: 4)**

MGHPRAIQPSVFFSPYDVHFLLYPIRCPYLKIGRFHIKLKGHLHFLFSFLFFFFETQSHSVTRLECGTISAHCNLCLPGSSNSPASASRV
AGTAGTCRRAQLIFVFLAEMGFHHVGRDGLDNLNVIHPPRSPKALGLQA

(-1)ORF (SEQ ID NO: 5)

MGHPRAIQPSVFFSPYDVHFLLYPIRCPYLKIGRFHIKLKGHLHFLFSFLFFFLRHSLTLSPGWSAVARSRLTATSASQVQVILLPQPPEW
LGLQARAAPAS

(+1)(-2)ORF (SEQ ID NO: 6)

MGHPRAIQPSVFFSPYDVHFLLYPIRCPYLKIGRFHIKLKGHLHFLFSFLFFF(F)

PTHL3**(wt)ORF (SEQ ID NO: 7)**

MQRRLVQQWSVAVFLLSYAVPSCGRSVEGLSRRLKRAVSEHQLLHDKGKSIQDLRRRFFLHHHLIAEIHAEIRATSEVSPNSKPSN
KNHPVRFGSDDEGRYLTQETNKVETYKEQPLKTPGKKKGKPGKRKEQEKKRRTSAWLDGVTGSGLEGDHLSDTSTSLELD
SRTALLWGLKKKKRKTTEEEHICN

(-1)ORF (SEQ ID NO: 8)

MQRRLVQQWSVAVFLLSYAVPSCGRSVEGLSRRLKRAVSEHQLLHDKGKSIQDLRRRFFLHHHLIAEIHAEIRATSEVSPNSKPSN
KNHPVRFGSDDEGRYLTQETNKVETYKEQPLKTPGKKKGKPGKRKEQEKKRRTSAWLDGVTGSGLEGDHLSDTSTSLELD
SRTALLWGLKKKKRKTTEEEHICN

(+1)(-2)ORF (SEQ ID NO: 9)

MQRRLVQQWSVAVFLLSYAVPSCGRSVEGLSRRLKRAVSEHQLLHDKGKSIQDLRRRFFLHHHLIAEIHAEIRATSEVSPNSKPSN
KNHPVRFGSDDEGRYLTQETNKVETYKEQPLKTPGKKKGKPGKRKEQEKKRRTSAWLDGVTGSGLEGDHLSDTSTSLELD
SRTALLWGLKKK(K)GQQKNTSYATNDLII

TGFbRII**(wt) (SEQ ID NO: 10)**

MGRGLLRLGLWPLHIVLWTRIASTIIPPHVQKSVNNDMIVTDNNNGAVKFPQLCKFCDFVRFSTCDNQKSCMSNCITSICKEPKQEVCVAV
WRKNDENITLETVC HDPKLPYHDFILEDAA SPKCIMKEKKPGETFFMCSSDECDNII FSEYNTSNPDLLVIFQVTGISLPL
VAISVIIIFCYRVNRQQQLSSTWETGKTRKLMFSEHCAILEDRSDISSTCANNINHNTELLPIELDTLVGKGRFAEVYKAKLKQNTS
EQFETVAVKIFPYEEYASWKTEKDIFSDINLKHENILQFLTAEERKTELGKQYWLITAFHAKGNLQEYLTRHVISWEDLRKLGSSLARGI
AHLHSDDHTPCGRPKMPIVHRLDNSSNILVKNDLTCCLCDFGLSLRDP TLVDDLANSQVGVTARYMAPEVLESRMNLENAESFKQT
DVYSMALVWEMTSRCNAVGEVKDYEPFGSKVREHPCVESMDNVLDRGRPEIPSFWL NHQGICMVCTLT ECWDHDPEARLT
AQCVAERFSELEHLDRLSGRSCSEEKIPEDGSLNTK

(-1)ORF (SEQ ID NO: 11)

MGRGLLRLGLWPLHIVLWTRIASTIIPPHVQKSVNNDMIVTDNNNGAVKFPQLCKFCDFVRFSTCDNQKSCMSNCITSICKEPKQEVCVAV
WRKNDENITLETVC HDPKLPYHDFILEDAA SPKCIMKEKKSLVRLSSCPVVALMSAM TSSSQKNITPAILT C

(+1)(-2)ORF (SEQ ID NO: 12/119)

MGRGLLRLGLWPLHIVLWTRIASTIIPPHVQKSVNNDMIVTDNNNGAVKFPQLCKFCDFVRFSTCDNQKSCMSNCITSICKEPKQEVCVAV
WRKNDENITLETVC HDPKLPYHDFILEDAA SPKCIMKEKK(K)AW

MACS**(wt)ORF (SEQ ID NO: 13)**

MGAQFSKTAKGEEAAERPGEAAVASSPSKANGQENGHVKGNDASPAAAESGAKEELQANGSAPAADKEEPAAAGSGAASPSS
AEKGEPAAAAPEAGASPVEKEAPAEGEAAEPGSATAAEGEAASAASSTSSPKAEDGATPSPSNETPKKKKKRFSFKSFKLSGFS
FFKKNKEAGEGGEAEAPAAEGGKDEAAGGAAAAAAEAGAASGEQAAAPGEEAAAGEEGAAGGDPQEAKPQEAAVAPAKEKPPASDE
TKAAEEPSKVEEKKAEEAGASAACAEAPSAAAGPGPAPPEQEAAPAEPPAAAASSACAAPSQEAQPECSPEAPPAAEAE

(-1)ORF (SEQ ID NO: 14)

MGAQFSKTAKGEEAAERPGEAAVASSPSKANGQENGHVKGNDASPAAAESGAKEELQANGSAPAADKEEPAAAGSGAASPSS
AEKGEPAAAAPEAGASPVEKEAPAEGEAAEPGSATAAEGEAASAASSTSSPKAEDGATPSPSNETPKKKRFSFKSFKLSGFS

(+1)(-2)ORF (SEQ ID NO: 15)

FIG. 2-2

MGAQFSKTAAKGEAAAERPGEAAVASSPSKANGQENGHVNVGDASPAAESEAELQANGSAPAADKEEPAAGSGAASPSS
AEKGEPEAAAPEAGASPVEKEAPAEGEAAEPGSATAAESEAASSTSSPKAEDGATPSPSNETPKKK(K)EALFLOEVFQAERL
LLQEEQEGGWRRR

TCF-4

(wt)ORF (**SEQ ID NO: 16**)

MPQLNGGGDDLGANDELISFKDEGEQEEKSSENSSAERDLADVKSSLVNESETQNNSSDSEAERRPPRSESFRDKSRESLEEA
AKRQDGGLFKGPPYGPFIIMPDLTSPYLPNGSLSPARTYLQMKWPLLDVQAGSLQSRQALKDARSPSPAIVSNKPVVQHPHH
VHPLTPLITYSNEHFTPNGNPPPHLPADVDPKTGI^{PRPPH}PDISPYPLSPGTVGQIPHPLGWLVPQQGQPVPITTGGFRHPYPTALT
VNASVSRFPFHMVPPHHTLHTTGI^{PHPA}IVTPTVKQESSQSDVGS^LHSSKHQDSKKEEEKKPHIKKPLNAFM^LYMKEMRAKVAEC
TLKESAAINQILGRRW^HALSREEQAKYYELARKERQLHMQLY^GPGWSARDNYGKKKRKRDKQPGETNEHSECFLNPCLSLPPITDLS
APKKCRARFGLDQQNNWC^GPCRKKCVRYI^QGE^GCSLSP^PSSDGSLLD^SPPPS^PNLLGSP^RDAKSQ^TQPLSLKPDPLAH
LSMMPPPP^PALLAEATHKASALCPNGALDLPPA^LQPAAPSSIAQPSTSWLHS^HSSL^AGTQPQPLSLVTKSLE

(-1)ORF (**SEQ ID NO: 17**)

MPQLNGGGDDLGANDELISFKDEGEQEEKSSENSSAERDLADVKSSLVNESETQNNSSDSEAERRPPRSESFRDKSRESLEEA
AKRQDGGLFKGPPYGPFIIMPDLTSPYLPNGSLSPARTYLQMKWPLLDVQAGSLQSRQALKDARSPSPAIVSNKPVVQHPHH
VHPLTPLITYSNEHFTPNGNPPPHLPADVDPKTGI^{PRPPH}PDISPYPLSPGTVGQIPHPLGWLVPQQGQPVPITTGGFRHPYPTALT
VNASVSRFPFHMVPPHHTLHTTGI^{PHPA}IVTPTVKQESSQSDVGS^LHSSKHQDSKKEEEKKPHIKKPLNAFM^LYMKEMRAKVAEC
TLKESAAINQILGRRW^HALSREEQAKYYELARKERQLHMQLY^GPGWSARDNYGKKKRKRDKQPGETNEHSECFLNPCLSLPPITDLS
APKKCRARFGLDQQNNWC^GPCRKKSAFATYKVAAASAHPLQMEA^Y

(+1)(-2)ORF (**SEQ ID NO: 18**)

MPQLNGGGDDLGANDELISFKDEGEQEEKSSENSSAERDLADVKSSLVNESETQNNSSDSEAERRPPRSESFRDKSRESLEEA
AKRQDGGLFKGPPYGPFIIMPDLTSPYLPNGSLSPARTYLQMKWPLLDVQAGSLQSRQALKDARSPSPAIVSNKPVVQHPHH
VHPLTPLITYSNEHFTPNGNPPPHLPADVDPKTGI^{PRPPH}PDISPYPLSPGTVGQIPHPLGWLVPQQGQPVPITTGGFRHPYPTALT
VNASVSRFPFHMVPPHHTLHTTGI^{PHPA}IVTPTVKQESSQSDVGS^LHSSKHQDSKKEEEKKPHIKKPLNAFM^LYMKEMRAKVAEC
TLKESAAINQILGRRW^HALSREEQAKYYELARKERQLHMQLY^GPGWSARDNYGKKKRKRDKQPGETNEHSECFLNPCLSLPPITDLS
APKKCRARFGLDQQNNWC^GPCRKK(K)VRS^LHTR

TAF1b

(wt)ORF (**SEQ ID NO: 19**)

IPAFFAGTVLQPFPEAALATRVPAVEAPAAPRLDLEESEEFKERCTQCAAVWGLTDEGKYYCTSCHNVTERYQEVNTDIPNT
QIKALNRGLKKKNTEKGWDWVYCEGFQYILYQQAEALKNLGVGPELKNDVLHNFWKRYLQSKQAYCKNPVY^TGRKPTVLEDNL
SHSDWASEPELLSDVCPFFLES^GAESQSDI^HTRKPF^VSKASQSET^SCSG^LD^GVEYSQR^EK^GI^VKM^TMPQ^TLAFCYLSLLWQ
REAITLSDLLRFVEEDH^IY^HIPY^INAFQHF^EQM^KLYGRDRG^IFG^IIES^WPDY^EDIYK^KTIEV^GTFLDLP^RFPD^IEDCYL^HPNILCM^KYLM^EV^N
LPDEMHSLTCHVV^KM^TG^MGEV^DFL^FDI^AMAK^AAV^KY^DV^QAV^VV^VL^KL^FL^MDD^SFE^WSL^SLA^EK^HNE^KN^KD^KP^WF^DFR^KW
YQIMKKAF^EKKQ^KW^EEE^AR^KY^LW^KSE^KP^LY^SF^VD^KP^VA^YK^KREM^VV^NLQK^QF^STL^DSTAG^KK^SP^SF^QFN^WTEED^TDR^TC
FHGHSLQGV^LK^EQ^GS^LL^TK^NS^LY^WL^ST^QK^FCR^W

(-1)ORF (**SEQ ID NO: 20**)

IPAFFAGTVLQPFPEAALATRVPAVEAPAAPRLDLEESEEFKERCTQCAAVWGLTDEGKYYCTSCHNVTERYQEVNTDIPNT
QIKALNRGLKKK^TI^LK^AG^IG^M^C^V^K^V^S^I^F^IN^K^Q^K^P

(+1)(-2)ORF (**SEQ ID NO: 21/120**)

IPAFFAGTVLQPFPEAALATRVPAVEAPAAPRLDLEESEEFKERCTQCAAVWGLTDEGKYYCTSCHNVTERYQEVNTDIPNT
QIKALNRGLKKK(K)Q^Y

AC-1

(wt)ORF (**SEQ ID NO: 22**)

MDTQKQI^HKTHNSKNQ^FFT^IFF^SVEFGKE^GTRKNFY^LLLSIGHYGRKSRRADLG^TADTADK^TEPECFAASWT^DPNPS^VTVSGAHS
TAVHQ

(-1)ORF (**SEQ ID NO: 23**)

MDTQKQI^HKTHNSKNQ^FFT^IFF^SC^QLN^IGR^KE^HA^KI^FFFF^QLD^TMD^GN^PG^ELT^LE^QTL^QI^KQ^SQ^NALL^PA^GPL^TQ^TPV

(+1)(-2)ORF (**SEQ ID NO: 24**)

MDTQKQI^HKTHNSKNQ^FFT^IFF^SP^VS

Sec63

(wt)ORF (**SEQ ID NO: 25**)

MAGQQFQYDDSGNTFFYFLTSFVGLIVIPATYYLWPRDQNAEQIRLK^NIRK^VYGR^CM^WY^RL^RL^KP^QP^NII^PV^KK^VLL^AG^WAL^FL^F
AYKVSKTDREYQ^EY^NP^YEV^LN^LD^GAT^VE^AE^IKKQ^YR^LL^KY^HPD^KG^GDEV^MF^MR^IA^KY^AAL^TDE^ESR^KN^WE^EF^GN^PD^GQ^AT^SF^F
GIALPAWIVDQKNSILVLLVYGLAFM^VILP^VVGS^WY^RS^IY^GD^QI^LR^TT^QI^YTY^FV^VK^TR^NMD^MK^RL^IM^VLAG^ASE^FDP^QY^NK^DAT^F
SRPTDN^LI^LP^QL^IR^EI^GS^IN^LKK^NE^PPL^TCP^YSL^KAR^VLL^LSH^LARM^KI^PE^TLE^ED^QQ^FML^KK^CP^ALL^QE^MV^NV^IC^QL^VM^AR^NRE^ERF^R
APTLASLEN^CM^KL^SQ^MAV^QGL^QQ^FK^SP^LQ^LPH^IE^EDN^LR^RV^SN^HK^YK^IKT^IQ^DL^VSL^KE^SDR^HLL^FLE^EK^YEV^MAV^LGS^FY^P
VTMDI^KSQVL^DDE^DSN^NIT^VGS^LVT^VL^VK^LR^QT^MA^EV^FE^KQ^SIC^AEE^QPA^ED^GQ^GGET^NK^NR^TK^GG^WQ^QK^SG^KP^KT^AK^SKK^R
PLKKKPT^VL^PQ^SK^QQ^KQ^QNG^VVG^NEA^VK^ED^{EE}E^VSD^KG^DS^{EE}E^TNR^DS^QE^KDD^GSD^RD^SREQ^DE^KQ^NK^DEA^EW^F
QELQQSI^QR^KE^ALL^ET^KS^IH^TP^VY^SL^FPEEK^QE^WW^LY^IADR^KE^QT^LIS^MP^YH^VC^TL^KD^TE^EV^EL^KF^PA^GK^PG^NY^QY^TV^FL^RS^D
SYMGLDQ^IK^PL^KL^EV^HE^AK^PV^PEN^HP^QW^DT^AE^IG^DE^DQ^ESE^GF^DS^{EE}EE^{EE}EE^{DD}D^D

(-1) 9er A-Repeat (**SEQ ID NO: 26**)

MAGQQFQYDDSGNTFFYFLTSFVGLIVIPATYYLWPRDQNAEQIRLK^NIRK^VYGR^CM^WY^RL^RL^KP^QP^NII^PV^KK^VLL^AG^WAL^FL^F
AYKVSKTDREYQ^EY^NP^YEV^LN^LD^GAT^VE^AE^IKKQ^YR^LL^KY^HPD^KG^GDEV^MF^MR^IA^KY^AAL^TDE^ESR^KN^WE^EF^GN^PD^GQ^AT^SF^F
GIALPAWIVDQKNSILVLLVYGLAFM^VILP^VVGS^WY^RS^IY^GD^QI^LR^TT^QI^YTY^FV^VK^TR^NMD^MK^RL^IM^VLAG^ASE^FDP^QY^NK^DAT^F
SRPTDN^LI^LP^QL^IR^EI^GS^IN^LKK^NE^PPL^TCP^YSL^KAR^VLL^LSH^LARM^KI^PE^TLE^ED^QQ^FML^KK^CP^ALL^QE^MV^NV^IC^QL^VM^AR^NRE^ERF^R
APTLASLEN^CM^KL^SQ^MAV^QGL^QQ^FK^SP^LQ^LPH^IE^EDN^LR^RV^SN^HK^YK^IKT^IQ^DL^VSL^KE^SDR^HLL^FLE^EK^YEV^MAV^LGS^FY^P
VTMDI^KSQVL^DDE^DSN^NIT^VGS^LVT^VL^VK^LR^QT^MA^EV^FE^KQ^SIC^AEE^QPA^ED^GQ^GGET^NK^NR^TK^GG^WQ^QK^SG^KP^KT^AK^SKK^R
PLKKKPT^VL^PQ^SK^QQ^KQ^QNG^VVG^NEA^VK^ED^{EE}E^VSD^KG^DS^{EE}E^TNR^DS^QE^KDD^GSD^RD^SREQ^DE^KQ^NK^DEA^EW^F
QELQQSI^QR^KE^ALL^ET^KS^IH^TP^VY^SL^FPEEK^QE^WW^LY^IADR^KE^QT^LIS^MP^YH^VC^TL^KD^TE^EV^EL^KF^PA^GK^PG^NY^QY^TV^FL^RS^D
SYMGLDQ^IK^PL^KL^EV^HE^AK^PV^PEN^HP^QW^DT^AE^IG^DE^DQ^ESE^GF^DS^{EE}EE^{EE}EE^{DD}D^D

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FIG. 2-3**(+1)/(-2) 9er A-Repeat (SEQ ID NO: 27)**

MAQQQFQYDDSGNTFFYFLTSFVGLIVIPATYYLWPRDQNAEQIRLKNIRKVVGRCMWYRLRLKPQPNIIPTVKKIVLLAGWALFLFLAYKVSKTDRREYQEYNPVEVLNLDPGATVAEIKKQYRLLSLKYHPDKGGDEVMFMRIAKAYAALTDEESRKNWEEFGNPDPQATSF
GIALPAWIVDQKNSILVLLVYGLAFMVILPVVVGWWYRSIRYSGDQILRTTQIYTYFVYKTRNMDMKRLIMVLAGASEFDPQYNKDAT
SRPTDNILIPQLIREIGSINLKKNEPPLTCPYSLKARVLLSLHARMKIPETLEEDQQFMLKKCPALLQEMVNIVCQLIVMARNREEREFR
APTLASLENCMKLSQMAVQGLQQFKSPLLQLPHIEEDNLRRVSNHKKYKIKTIQDLSLKESDRHTLLHFLEDEKYEEVMAVLGSFPY
VTMDIKSQVLDDEDSNINITVGLVTKLRTQTMMAEVFEKEQSICAAECPAEDGQGETNKNRTKGGWQQ
KSKGPKKTAKS(K)ETFKKKVTCATTVKATETKAGKWSRWE

(-1) 10er A-Repeat (SEQ ID NO: 28)

MAQQQFQYDDSGNTFFYFLTSFVGLIVIPATYYLWPRDQNAEQIRLKNIRKVVGRCMWYRLRLKPQPNIIPTVKKIVLLAGWALFLFLAYKVSKTDRREYQEYNPVEVLNLDPGATVAEIKKQYRLLSLKYHPDKGGDEVMFMRIAKAYAALTDEESRKNWEEFGNPDPQATSF
GIALPAWIVDQKNSILVLLVYGLAFMVILPVVVGWWYRSIRYSGDQILRTTQIYTYFVYKTRNMDMKRLIMVLAGASEFDPQYNKDAT
SRPTDNILIPQLIREIGSINLKKNEPPLTCPYSLKARVLLSLHARMKIPETLEEDQQFMLKKCPALLQEMVNIVCQLIVMARNREEREFR
APTLASLENCMKLSQMAVQGLQQFKSPLLQLPHIEEDNLRRVSNHKKYKIKTIQDLSLKESDRHTLLHFLEDEKYEEVMAVLGSFPY
VTMDIKSQVLDDEDSNINITVGLVTKLRTQTMMAEVFEKEQSICAAECPAEDGQGETNKNRTKGGWQQ
KSKGPKKTAKS(K)KKPLKKNLHLCYHSQSNNRNSRQMSLGMKLQ

(+1)/(-2) 10er A-Repeat (SEQ ID NO: 29)

MAQQQFQYDDSGNTFFYFLTSFVGLIVIPATYYLWPRDQNAEQIRLKNIRKVVGRCMWYRLRLKPQPNIIPTVKKIVLLAGWALFLFLAYKVSKTDRREYQEYNPVEVLNLDPGATVAEIKKQYRLLSLKYHPDKGGDEVMFMRIAKAYAALTDEESRKNWEEFGNPDPQATSF
GIALPAWIVDQKNSILVLLVYGLAFMVILPVVVGWWYRSIRYSGDQILRTTQIYTYFVYKTRNMDMKRLIMVLAGASEFDPQYNKDAT
SRPTDNILIPQLIREIGSINLKKNEPPLTCPYSLKARVLLSLHARMKIPETLEEDQQFMLKKCPALLQEMVNIVCQLIVMARNREEREFR
APTLASLENCMKLSQMAVQGLQQFKSPLLQLPHIEEDNLRRVSNHKKYKIKTIQDLSLKESDRHTLLHFLEDEKYEEVMAVLGSFPY
VTMDIKSQVLDDEDSNINITVGLVTKLRTQTMMAEVFEKEQSICAAECPAEDGQGETNKNRTKGGWQQ
KSKGPKKTAKS(K)KKPLKKNLHLCYHSQSNNRNSRQMSLGMKLQ

Caspase 5**(wt)ORF (SEQ ID NO: 30)**

MFKGILQSGLDNFVINHMLKNNVAGQTSIQTLPNTDQKSTSVKKDHNKKKTVKMLEYLGDVLHGTVNLYAKHDVLTKEEEKKK
DAIKEDKALIVDLSLRKRNRAVQHMQFTQTLNNMDQKITSVKPLLQIEAGPPESAESTNILKCPREEFLRLCKNNHDEIYPIKKREDRRRLA
LIICNTKFDLHPARNGAHYDIVGMKRLLQGLGTYVDEKNLTARDMESVLRFAARPEHKSSDSTFLVMSHGILEGICGTAHKKKPD
VLLYDTIFQFQINRNCLSLKDQPKVIIQACRGEKHGELWVRSPLASLAVISSQSSENLEADSVCVCIHEEKDFIAFCSTPHNVSWRDR
TRGSIFITELITCFQKYSCCCHLMEIFRKVQKSFEVQPKAQMPTIERATLTRDFYLPFGN

(-1)ORF (SEQ ID NO: 31)

MFKGILQSGLDNFVINHMLKNNVAGQTSIQTLPNTDQKSTSVKKDHNKKQLCWNTWAKMFFMVFLIIWQNTMF

(+1)/(-2)ORF (SEQ ID NO: 32)

MFKGILQSGLDNFVINHMLKNNVAGQTSIQTLPNTDQKSTSVKKDHNKK(K)NS

AIM2**(wt)ORF (SEQ ID NO: 33)**

MESKYKEIILLTGLDNITDEELDRFKFFLSDEFNIATGKLHTANRIQVATLMIQNAGAVSAVMKTRIFQKLNYMILLA
KRLQEEKEVKDKQYKSVTKPKPLSQAEMSPAASAAIRNDVAKQRAAPKVSHPVKPEQKQMV
AQQESIREGFQKRCPLVMVLKAKKPFTETQEGKQEMF
HATVATEKEFFFVVFNTLLDKFIPKRIIIARYYRHSGFLEVSASRVLDAESDQKVNVPLNIIRKAGETPKINTLQTQPLGTIVGLFV
VQKVTEKKKNILFDLSNTGKMEVLGVRNEDTMCKEGDKVRLFTTLSKGKQLTSGVHSTIKVIAKAKKK

(-1)ORF (SEQ ID NO: 34)

MESKYKEIILLTGLDNITDEELDRFKFFLSDEFNIATGKLHTANRIQVATLMIQNAGAVSAVMKTRIFQKLNYMILLA
KRLQEEKEVKDKQYKSVTKPKPLSQAEMSPAASAAIRNDVAKQRAAPKVSHPVKPEQKQMV
AQQESIREGFQKRCPLVMVLKAKKPFTETQEGKQEMF
HATVATEKEFFFVVFNTLLDKFIPKRIIIARYYRHSGFLEVSASRVLDAESDQKVNVPLNIIRKAGETPKINTLQTQPLGTIVGLFV
VQKVTEKKKNILFDLSNTGKMEVLGVRNEDTMCKEGDKVRLFTTLSKGKQLTSGVHSTIKVIAKAKKKHREVKRTNSSQLV

(+1)/(-2)ORF (SEQ ID NO: 35)

MESKYKEIILLTGLDNITDEELDRFKFFLSDEFNIATGKLHTANRIQVATLMIQNAGAVSAVMKTRIFQKLNYMILLA
KRLQEEKEVKDKQYKSVTKPKPLSQAEMSPAASAAIRNDVAKQRAAPKVSHPVKPEQKQMV
AQQESIREGFQKRCPLVMVLKAKKPFTETQEGKQEMF
HATVATEKEFFFVVFNTLLDKFIPKRIIIARYYRHSGFLEVSASRVLDAESDQKVNVPLNIIRKAGETPKINTLQTQPLGTIVGLFV
VQKVTEKKKNILFDLSNTGKMEVLGVRNEDTMCKEGDKVRLFTTLSKGKQLTSGVHSTIKVIAKAKK(K)NIK

SLC23A1**(wt)ORF (SEQ ID NO: 36)**

MMGIGKNTTSKSMEAGSSTEGKYEDEAKHPAFFTLPVVINGGATSSGEQDNEDTELMAIYTTENGIAEKSSLAETLDSTGSLDPQRS
DMIYTIEDVPPWYLCIFLGLQHYLTCFSGTIAVPFLADAMCVGYDQWATSQLIGTIFFCVGITLLQTTFCRCLPLFQTSAFAFLAPARA
ILSLDKWKCNTTDVSVANGTAELLHTEHIWYPRIREIQGAIIMSSLIEVVIGLLGLPGALLKYIGPLTITPTVALIGLSGFQAAGERAGKHW
GIAMLTIFLVLFSQYARNVFKPLPIYKSKKGWTAYKLQLFKMFPIILAILVSWLLCFIFTVTDVFPDDSTKYGFYARTDARQGVLLVAPW
FKVPPYFPFWGLPTVSAAGVIGMSAVVASIIESIGDYYACRLSCAPPPIHAINRGIFVEGLSCVLGDFGTGNGSTSSSPNIGVLGIT
VGSRRVIQCGAALMLALGMIGKFSALFSLPDPVLGALFCFTLFGMITAVGLSNLQFIDLNSSRNLFVLGFSIFFGLVLPSYLRQNPLVTG
TGIDQVLNVLLTTAMFVGGCVAFILENTIPGTPERGIRKWWKGVGKGNKSLDMESYNLPFGMNIKKYRCFSYLPISPTFVGTYWK
GLRKSDNSRSSDEDSQATG

(-1)ORF (SEQ ID NO: 37)

MMGIGKNTTSKSMEAGSSTEGKYEDEAKHPAFFTLPVVINGGATSSGEQDNEDTELMAIYTTENGIAEKSSLAETLDSTGSLDPQRS
DMIYTIEDVPPWYLCIFLGLQHYLTCFSGTIAVPFLADAMCVGYDQWATSQLIGTIFFCVGITLLQTTFCRCLPLFQTSAFAFLAPARA
ILSLDKWKCNTTDVSVANGTAELLHTEHIWYPRIREIQGAIIMSSLIEVVIGLLGLPGALLKYIGPLTITPTVALIGLSGFQAAGERAGKHW
GIAMLTIFLVLFSQYARNVFKPLPIYKSKKGWTAYKLQLFKMFPIILAILVSWLLCFIFTVTDVFPDDSTKYGFYARTDARQGVLLVAPW
FKVPPYFPFWGLPTVSAAGVIGMSAVVASIIESIGDYYACRLSCAPPPISTQ

(+1)/(-2)ORF (SEQ ID NO: 38)

FIG. 2-4

MMIGKNTTSKSMEAGSSTEGKYEDEAKHPAFFTLPVVINGGATSSGEQDNEDTELMAIYTTENGIAEKSSLAETLDSTGSLDPQRS
 DMIYTIEDVPPWYLCIFGLQHYLTFCSGTIAVPFLLADAMCVGYDQWATSQLIGTIFFCVGIFTLLQTTFCRLPLFQTSAFLAPARA
 ILSLDKWKCNTTDVSVANGTAELLHTEHIWYPRIREIQQGAIMSSLIEVVIGLLGLPGALLKYIGPLTITPTV рАLIGLSGFQAAGERAGKHW
 GIAMLTIFLVLLFSQYARNVKFPLIYKSKKGWTAYKLQLFKMFPILAILVSWLLCFIFTVDVFPPDSTKYGFYARTDARQGVLLVAPW
 FKVPYPFWGLPTVSAAGVIGMLSAAVVASIIIESIDYYACARLSCAPP
 (P)HPRNKQGNFRGRPLLC

ABC1**(wt)ORF (SEQ ID NO: 39)**

MPKAPKQQPPEPEWIGDGESTSPSDKV/KKGKKDKKKTFFEEELAVEDKQAGEEEKVLKEKEQQQQQQQQKKRDRTRKGRR
 KKDWDDEGEEKELMERLKKLSPVTSDEEDEVAPKPRGGKKTGGNVFAALIQDQSEEEEEEKHPKPAKPEKNRINKAVSEEQQ
 PALGKKGKKEEKSGKAKPQNFKAALDNEEEDKEEEIKEKEPKQGKEAKKAQEMEYERQVASLKAANAAENDFSVSQAEMSSR
 QAMLENASDIEKLFNSIAHGKELFVNADLYIVAGRRYGLVGPNGKGKTLKHIANRALSIPPNDVLLCEQEVADETPAVQAVLRAD
 TKRLKLLEERRLQQGLEQGDDTAERLEKVYEELRATGAAAEEAKARRILAGLGFDPREMQRPTQKFSGGWRMRVSLARALFMEP
 TLLMLDEPTNHLDLNAVIWLNYYLQGWRKTLIVSHDQGFDDVCTDIHLDAQRLHYYRGNYMTFKKMYQQKQKELLKQYEQKQKEL
 KELKAGGKSTKQAEKQTKEALTRQQKCRRKQNQDEESQEAPELLKRPKYETVRFTFPDPPLSPPVGLHGVTFGYQGQKPLFKNL
 DFGIDMDSRICIVGPNGVKLNTGKLTPTHEMRKHNRLKIGFFNQQYAEQLRMEETPTEYLQRGFNLQYQDARKCLGRFGLE
 SHAHTIQCKLSSGQKARVVFAELACREPDLIILDEPTNLDIESIDALGEAINEYKGAVVSHDARLITETNCQLWVVEEQSVSQIDG
 DFEDYKREVLEALGEVMVSRPRE

(-1)ORF (SEQ ID NO: 40)

MPKAPKQQPPEPEWIGDGESTSPSDKV/KKGKKDKKKTFFEEELAVEDKQAGEEEKVLKEKEQQQQQQQQKKSEIPEKAGGR
 RMWMMMEKRKSSWSVLRSSQCOPVMRRMKYPPQNPAEGRKPRVVMFLQP

(+1)(-2)ORF (SEQ ID NO: 41)

MPKAPKQQPPEPEWIGDGESTSPSDKV/KKGKKDKKKTFFEEELAVEDKQAGEEEKVLKEKEQQQQQQQQKK(K)ARYPKRQA
 EEGCG

HSPC259**(wt)ORF (SEQ ID NO: 42)**

SPDYFPQISSQFGTVKEK
 MEKIFISSSTKAEGKGISPFEAPINTQAPPEKGKEAVVQEPERSWFQTKEERKKEKIAKALQEFDLALRGKKKRKKFMKDAKKKGEMT
 AEERSQFEILKAQMFAERLAKRNRRAKRARAMPEEEPVRGPAKKQKGKKSVDDEELNTSKALKQYRAGPSFEERKQLGLPHQR
 RGGNFKSNPDTRGGSSCRGLKKFMGAALKSLPCGKSSWLVCLFSICLKKQKQKTLWCAGGMVRSYFPKHVQCSPFLISFHMTIL
 NGSIFGKRE

(-1)ORF (SEQ ID NO: 43)

MEKIFISSSTKAEGKGISPFEAPINTQAPPEKGKEAVVQEPERSWFQTKEERKKEKIAKALQEFDLALRGKKKRKKFMKDAKKKGEMT
 AEERSQFEILKAQMFAERLAKRNRRAKRARAMPEEEPVRGPAKKQKGKKSVDDEELNTSKALKQYRAGPSFEERKQLGLPHQR
 RGGNFKSNPDTRGGSSCRGLKKFMGAALKSLPCGKSSWLVCLFSICLKKNNKKHFGVWWYVAIFLSMSVNLPSC

(+1)(-2)ORF (SEQ ID NO: 44)

MEKIFISSSTKAEGKGISPFEAPINTQAPPEKGKEAVVQEPERSWFQTKEERKKEKIAKALQEFDLALRGKKKRKKFMKDAKKKGEMT
 AEERSQFEILKAQMFAERLAKRNRRAKRARAMPEEEPVRGPAKKQKGKKSVDDEELNTSKALKQYRAGPSFEERKQLGLPHQR
 RGGNFKSNPDTRGGSSCRGLKKFMGAALKSLPCGKSSWLVCLFSICLKK(K)TKTNNTLVWWYGT

Bax**(wt)ORF (SEQ ID NO: 45)**

MDGSGEQRGGGPTSSEQIMKTGALLLQGFIQDRAGRMGEAPELALDPVPQDASTKKLSECLKRIGDELDNSMELQRMIAAVDTD
 SPREVFFRVAADMFSQDNFNWGRVVALFYFASKLVLKALCTKVPELIRTMGWTLDLRLERLLGWIQDQGGWDGLLSYFGPTWQT
 VTIFVAGVLTASLTWKKMG

(-1)ORF (SEQ ID NO: 46)

MDGSGEQRGGGPTSSEQIMKTGALLLQGFIQDRAGRMGRHPSWPWTRCLMRPPRS

(+1)(-2)ORF (SEQ ID NO: 47)

MDGSGEQRGGGPTSSEQIMKTGALLLQGFIQDRAGRMGG(G)GTRAGPGPGASGCVHQEAERVSQAHRGRTGQ

TCF6L1**(wt)ORF (SEQ ID NO: 48)**

MAFLRSMWGVLSALGRSGAELCTGCGSRLRSPFSFVYLPWFSSVLASCPKKPVSSYLRFSKEQLPIFKAQNPDAKTTELIRRIAQR
 WRELPDSKKKIYQDAYRAEWQVYKEEISRFKEQLTPSQIMSLEKEIMDKHLKRKAMTKKELTLLGKPKRPRSAVNVAERFQEAK
 GDSPQEKLTKVKENWKNLSDSEKELYIQHAKEDETRYHNEMKSWEEQMIEVGRKDLLRRTIKKQRKYGAEEC

(-1)ORF (SEQ ID NO: 49)

MAFLRSMWGVLSALGRSGAELCTGCGSRLRSPFSFVYLPWFSSVLASCPKKPVSSYLRFSKEQLPIFKAQNPDAKTTELIRRIAQR
 WRELPDSKKKIYQDAYRAEWQVYKEEISRFKEQLTPSQIMSLEKEIMDKHLKRKAMTKKKS

(+1)(-2)ORF (SEQ ID NO: 50)

MAFLRSMWGVLSALGRSGAELCTGCGSRLRSPFSFVYLPWFSSVLASCPKKPVSSYLRFSKEQLPIFKAQNPDAKTTELIRRIAQR
 WRELPDSKKKIYQDAYRAEWQVYKEEISRFKEQLTPSQIMSLEKEIMDKHLKRKAMTKK(K)RNTAWTKTKTSFSL

FTL3L**(wt)ORF (SEQ ID NO: 51)**

MTVLAPAWSPPTYLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKT
 VAGSKMQLLERVNTEIHFTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSLPPWSPRPLE
 ATAPTAQPPPLLLLPVGLLLAAWCLHWQRTRRTPRGEQVPPVSPQDLLLVEH

(-1)ORF (SEQ ID NO: 52)

MTVLAPAWSPPTYLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKT
 VAGSKMQLLERVNTEIHFTKCAFQ
 PPPAVFASRPTSPASCRRPPSSWWR

FIG. 2-5**(+1)(-2)ORF (SEQ ID NO: 53)**

MTVLAPAWSPPTYLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKT
VAGSKMKGGLERVNTEIHFTKCAFQ
PP(P)QLSSLRPDQHLPAGDLRAAGGAEALDHSPELLPVPGAAVSAR

OGT**(wt)ORF (SEQ ID NO: 54)**

MLQGHFWLVREGIMISPSSPPPPNLFFFPLQIFPFPTSFPSHLLSLTPPKACYLKAIETQPNFAVWSNLGCVFNAQGEIWLAIHHFE
KAVTLDNFNLDAYINLGVLKEARIFDRAVAAYLRLALSLSPNHAVVHGNLACVYYEQGLIDLAIDTYRRAIELQPHFPDAYCNLANALKE
KGSVAEAEDCYNTALRLCPTHADSLNNLNIKREQGNIEEAVRLYRKALEVFPFEEAAHSNLASVLQQQGKLQEALMHYKEAIRISPTF
ADAYSNMGNTLKEMQDVQGALQCYTRAQINPAFADAHNSNLASIHKDSGNIPAEIASYRTALKLPDFPDAYCNLAHCLQIVCDWTDY
DERMKKLVLIVADQLEKNRPLSVPHHSMLYPLSHGRKAIAERHGNLCLDKLSDGRLRVGYVSSDFGNHPT
SHLMSQIPGMHNPDKFEVFCYALSPDDGTNFRVKVMAEANHFDLNSQIPNGKAADRIHQDGIIHLVNMGYTKGARNELFALRPAPI
QAMWLGYPGTSGALFMDIITDQETSPAEVAEQYSEKLAYMPHTFIGDHNMFPHLKKAVIDFKSNHGYIDNRIVLNGIDLKAFLDS
LPDVKIVKMKCPDGGDNADSSNTALNMPVIPMNTIAEAVIEMINRGQIQTINGFSISGLATTQINNKAATGEEVPRITIIVTRRSQYGLP
EDAIVYCNFNQLYKIDPSTLQMWANILKRVPSVWLRLRPAVGEPNQQYAQNMGLPQNRIFSPVAPKEEHVRRGQLADVCLDTPL
CNGHTGMDVLWAGTPMTMPGETLASRVAQSLTLCGLELIAKNRQEYEDIAVKLTDLEYLKKVRGKVKWQRISPLFNTKQYT
MELERLYLQMWEHYAAGNKPDMHMKPVEVTEA

(-1)ORF (SEQ ID NO: 55)

MLQGHFWLVREGIMISPSSPPPPNLFFS~~LYKFSPFPLPPFPPIFFH~~

(+1)(-2)ORF (SEQ ID NO: 56)

MLQGHFWLVREGIMISPSSPPPPNLFF(F)PFTNFPLSLYLLSLPSSFINPS

ELAVL3**(wt)ORF (SEQ ID NO: 57)**

MESQVGGPAGRPAGQRLPLGNGATDDSKTNLIVNYLPQNMQTQDEFKSLFGSIGDIESCKLVRDKITGQSLGTYGFVNYSDPNDADKA
INTLNGLKLQQTKTIVSARPPSSASRDNALVSGLPKTMQSKEQQLFSQYGRITSRILVDQVTGVSRGVGFIRFDKRIEAEAIKGLN
GQKPLGAREPITVKFANNPQSKTGTQALLTHLYQSSARRYAGPLHHQTORFRLDNLLNMAVAKRFSPIADGMSGLAGVGLSGGAAG
GWCIFVYNLSPEPDQSVLWQLFGPGAVTNVKIRDFTNKCKGFGMTMTNYDEAAMAIASLNGYRLGQRLVQSFKTSQHKA

(-1)ORF (SEQ ID NO: 58)

MESQVGGARPAGLPGNQHSLVQMEPLTTARPTSSSTTCRPT

(+1)(-2)ORF (SEQ ID NO: 59)

MESQVGG(G)PGRPACPTATPWYKWSH

MAC30X**(wt)ORF (SEQ ID NO: 60)**

LFSHQRVQAQPTDYGGSFTRRCVEWLLGLYFLSHIPITLFMDLQAVVPRELYPVEFRNLLKWAKEFKDPLLQEPPAWFKSFLFCELV
FQLPFFPIATYAFLGSKCWIRTPAIYSVHTMTLILSTFLFEDFSKASGFKGQRPETLHERLTVSVYAPYLLIPFILLIFMLRSPYYKY
EEKRKKK

(-1)ORF (SEQ ID NO: 61)

LFSHQRVQAQPTDYGGSFTRRCVEWLLGLYFLSHIPITLFMDLQAVVPRELYPVEFRNLLKWAKEFKDPLLQEPPAWFKSFLFCELV
FQLPFFPIATYAFLGSKCWIRTPAIYSVHTMTLILSTFLFEDFSKASGFKGQRPETLHERLTVSVYAPYLLIPFILLIFMLRSPYYKY
EEKRKKK~~NEGNH~~WPRVEMPTGWLLVGYIQEHCSEPTSSAAFETLAAMHKSKMVGTSMSNPHLLPFFFFF

(+1)(-2)ORF (SEQ ID NO: 62)

LFSHQRVQAQPTDYGGSFTRRCVEWLLGLYFLSHIPITLFMDLQAVVPRELYPVEFRNLLKWAKEFKDPLLQEPPAWFKSFLFCELV
FQLPFFPIATYAFLGSKCWIRTPAIYSVHTMTLILSTFLFEDFSKASGFKGQRPETLHERLTVSVYAPYLLIPFILLIFMLRSPYYKY
EEKRKKK~~(K)MKETT~~GP

SLC4A3**(wt)ORF (SEQ ID NO: 63)**

MANGVPPGGASPLPQVRVPLLEPPPLSPDVEEEEDDLGKTLAVSRFGDLISKPPAWDPEKPSRSYSERDfefhrhtshhthhplsa
RLPPPHKLRRLPPTSARHTRRKRKEKTSAPPSEGTPPIQEEGGAGVDEEEEEEEEGESEAEVPEPPPSGTPQAKFSIGSDEDD
SPGLPGRAAVTKPLPSVGPHTDKSPQHSSSSPSRARASRLAGEKSRPWSPSASYDLERLCPGSALNPQGPEQQVPTDEAEAQ
MLGSADLDDMKSHRLEDNPVGRRHLVKKPSRTQGGGRGSPSGLAPILRRKKKKKKLDRRPEHVVELNELMDRSQEPHWRETARW
IKFEEDVEEETERWGKPHVASLFSRSLLELRRTIAHGAALLDEQTTLPGIAHLVVTMIVSDQIRPEDRASVRLTLLKHSHPNDDKDS
GFFPRNPSSSSMNSVGNHHPTPSHGPDAVPTMADDLGEPAVLPHDPAKEKPLHMPGGDGHRGKSKLLEKIPEDAETVVL
VGCFVFPLEQPAAAVFLVNEAVLLESLEVPPVVRFLFVMLGSPSHTSTDYHELGRSIAITLMSDKLFLHEAAYQADDRQDLSAISEFLDG
SIVIPPSVEVGRDPLLRSAFAFQRELLRKRREQTKVEMTRGTYATPGKELSLELGGSEATPEDDPLRTGSVFGGLVRDVRRRY
HYPSDLRDLHSQCVAALFYFAALSPAIFTGCLLGEKTEGLMGVSELIYSTAVLGVLFSLGAQPLLGVFGSPLLVFEAAFFKFCRA
QDLEYLTGRVWVGLWLVVFVLAVALAAEGSFLVRYISPFTQEIAFLISLIFYETFYKLYKVFTEHPLPFYPPEGALEGSLAAGLEPNGS
ALPPTEGPPSPRNPQNTALLSLILMLGTFIIFLRFKFRNSRFLGGKARRIIGDFGIPISILVMVLVDYISITDTYQKLTVPTGLSVTSPDK
RSWFIPPLGSARPFPWWMM/AAAVPALLVLILIFMETQITALIVSQKARRIIGDFGIPISILVMVLVDYISITDTYQKLTVPTGLSVTSPDK
NALTVMRATAIPGDKPOIQEVREQRVTGLVLIASLVLGSIIVMGAVLRRIPAVLFGIFLYMGVTSLSQIQLSQRLLLIMPAKHHPEQPYVT
KVKTWRMHLFTCQLGCIALLWVVKSTAASLAFFLMLTVPRLHCLLPRFLFQDRELQALDSEDAEPNFDEDGQDYEINELHMPV

(-1)ORF (SEQ ID NO: 64)

MANGVPPGGASPLPQVRVPLLEPPPLSPDVEEEEDDLGKTLAVSRFGDLISKPPAWDPEKPSRSYSERDfefhrhtshhthhplsa
RLPPPHKLRRLPPTSARHTRRKRKEKTSAPPSEGTPPIQEEGGAGVDEEEEEEEEGESEAEVPEPPPSGTPQAKFSIGSDEDD
TVQASLGGLSPSPCPRWAHTLTRAPSTPAAPPAPGPGPPDSLGRKAGPGAAHRRPVMTCGSDCAQAVPWATQVVGSSRCPQMRR
PRCWVLQWT

(+1)(-2)ORF (SEQ ID NO: 65)

MANGVPPGGASPLPQVRVPLLEPPPLSPDVEEEEDDLGKTLAVSRFGDLISKPPAWDPEKPSRSYSERDfefhrhtshhthhplsa
RLPPPHKLRRLPPTSARHTRRKRKEKTSAPPSEGTPPIQEEGGAGVDEEEEEEEEGESEAEVPEPP(P)LRDPTEGKVHLWK

FIG. 2-6

PRKDC

(wt)ORF (SEQ ID NO: 66)

MAASAGVRCSSLRLQETLSAADRCGAALAGHQIRGLGQECVLSSPAVLALQTSVLFSRDFGLLVFVRKSLNSIEFRECREEILKFL
CIFLEKMGQKIAPIYSVEIKNTCTSVTKDRAAKCKIPALDLIKLLQTFRSSRLMDEFKIGELFSKFYGELALKKIPDTVLEKVYELLGLL
GEVHPSEMINNAENLFR AFLGELKTQMTSAVREPKLPVLAGCLKGSSLLCNFTKSMEEDPQTSREIFNFVLAIRPQIDLKRYAVPSA
GLRLFALHASQFSTCLLDNYVSLFVEVLLKWC AHTNVELKKAALSALESFLKQVSNMVAKNAEMHKNKLQYFMEQFYGIIRNVDNSNNKE
LSIAIRGYGLFAGPCKVINA KDVDPMYV E LIQRCQMF LTQDTGDDRVYQMPFLQSVASVLLYLDTVEVYTPVLEHLVVMQIDSFP
QYSPKMQLVCCRAIVKFLALAAGPVL RNCISTVHQGLIRICSKPVVLPKGPESESEDHRSAGEVRTGKWKVPTYKDYV/DLFRHLL
SSDQMMDSILADEAFFSVN SSESLSN HLLYDEFVKSVLKIVEKLDLTLIEQTVGEQENGDEAPGVWMIPTSDPAANLHPAKPKDFAFI
NLVEFCREIPEKQAEFFEPWVYFSYELILQSTRPLISGFYKLLSITVRNAKKIKYFEGS

(-1)ORF (SEQ ID NO: 67)

MAASAGVRCSSLRLQETLSAADRCGAALAGHQIRGLGQECVLSSPAVLALQTSVLFSRDFGLLVFVRKSLNSIEFRECREEILKFL
CIFLEKMGQKIAPIYSVEIKNTCTSVTKDRAAKCKIPALDLIKLLQTFRSSRLMDEFKIGELFSKFYGELALKK~~Y~~Q/QF

(+1)(-2)ORF (SEQ ID NO: 68)

MAASAGVRCSSLRLQETLSAADRCGAALAGHQIRGLGQECVLSSPAVLALQTSVLFSRDFGLLVFVRKSLNSIEFRECREEILKFL
CIFLEKMGQKIAPIYSVEIKNTCTSVTKDRAAKCKIPALDLIKLLQTFRSSRLMDEFKIGELFSKFYGELALKK(K)TRYSRKS

UVRAG

(wt)ORF (SEQ ID NO: 69)

MSASASVGGPVPQPPP G PAA ALPPG SAAR ALH VELPSQ Q RRL RHL R NIA A R N I V N R N G H Q L L D T Y F T L H L C S T E K I Y K E F Y R S E V I K N
S L N P T W R S L D F G I M P D R L D T S V C F V V K I W G G K E N I Y Q L L I E W K V C L D G L K Y L G Q Q I H A R N Q N E I I F G L N D G Y Y G A P F E H K G Y S N A Q K
T I L L Q V D Q N C V R N S Y D V F S L L R L H R A Q C A I K Q T Q V T V Q K I G K E I E E K L R L T S N E L K K V V / A C S
K Q Q I A L Q D K G S A F S A E H L K L Q L Q K E S L N E L R K E C T A K R E F L K T N A Q L T I R C R Q L L S E L S Y I Y P I D L N E H K D Y F V C G V K L P N S E D F Q A K
D D G S I A V A L G Y T A H L V V S M I S F F L Q V P L R Y P I I H K G S R T I K D N I N D K L T E K E R E F P L Y P K G G E K L Q F D Y G V Y L N K N I A Q L R Y Q H G L G T P
D L R Q T L P N L K N F M E H G L M V C R D R H T S S A I P V P K R Q S S I F G G A D V G F S G G I P S P D K G H R K R A S S E N E R L Q Y K T P P P S Y N S A L A Q P V T
T V P S M G E T E R K I T S L S S S L D T S L D F S K E N K K K G E D L V G S L N G G H A N V H P S Q E Q G E A L S G H R A T V N G T L L P S E Q A G S A V Q L P G E F H
P V S E A E L C C T V Q A E E I I G L E A Q V S P Q V I S

(-1)ORF (SEQ ID NO: 70)

MSASASVGGPVPQPPP G PAA ALPPG SAAR ALH VELPSQ Q RRL RHL R NIA A R N I V N R N G H Q L L D T Y F T L H L C S T E K I Y K E F Y R S E V I K N
S L N P T W R S L D F G I M P D R L D T S V C F V V K I W G G K E N I Y Q L L I E W K V C L D G L K Y L G Q Q I H A R N Q N E I I F G L N D G Y Y G A P F E H K G Y S N A Q K
T I L L Q V D Q N C V R N S Y D V F S L L R L H R A Q C A I K Q T Q V T V Q K I G K E I E E K L R L T S N E L K K V V / A C S

(+1)(-2)ORF (SEQ ID NO: 71)

MSASASVGGPVPQPPP G PAA ALPPG SAAR ALH VELPSQ Q RRL RHL R NIA A R N I V N R N G H Q L L D T Y F T L H L C S T E K I Y K E F Y R S E V I K N
S L N P T W R S L D F G I M P D R L D T S V C F V V K I W G G K E N I Y Q L L I E W K V C L D G L K Y L G Q Q I H A R N Q N E I I F G L N D G Y Y G A P F E H K G Y S N A Q K
T I L L Q V D Q N C V R N S Y D V F S L L R L H R A Q C A I K Q T Q V T V Q K I G K E I E E K L R L T S N E L K K V V / K

MSH3

(wt)ORF (SEQ ID NO: 72)

MSRRKPASGGLAASSSAPARQAVLSRFFQSTGSLKSTSSSTGAADQVDPGAAAAAAAAAAPPAPPAPAFPPQLPPHVATEIDRR
KKRPLENDGPVKKVKKVQQKEGGSDLGMSGNSEPPKCLRTRNVSKSLEKLFECFCDSALPQSRVQTESLQERFAVLPKCTDFDDI
SLLHAKNAVSSEDSKRQINQKD TLF DLSQFGSSNTSHENLQKTASKSANKRSKSIYTPLELQYIEMKQQHKDAVLCECGYKYRFFG
E D A E I A A R E L N I Y C H L D H N F M T A S I P T H R L F V H V R R L V A K G Y K V G V V K Q T E A L K A I G D N R S S I F S R K L T A L Y T K S T L I G E D V N P L I K L D
D A V N V D E I M T D T S T S Y L L C I S E N K E N V R D K K G N I F I G I V G V Q P A T G E V V F D S F Q D S A R S E L T R M S S L Q P V E L L L P S A L S E Q T E A L I H
R A T S V S V Q D D R I V R E V M D N I Y F E Y S H A F Q A V T E F Y A K D T V D I K G S Q I I S G I V N L E K P V I C S L A I I K Y L K E F N L E K M L S K P E N F K Q L S S K M
E F M T I N G T T L R N L E I L Q N Q D M T K G S L L W V L D H T K T S F G R R K L K K W V T Q P L L K L R E I N A R L D A V S E V L H S E S S V F G Q I E N H L R K L P D I
G R G L C S I Y H K K C S T Q E F F L I V K T L Y H L K S E F Q A I P A V N H I Q S D L L R T V I L E I P E L L S P V E H Y L K I L N E Q A A K V G D K T E L F K D L S D F P L I K K
R K D E I Q G V I D E I R M H L Q E I R K I L K N P S A Q Y V T V S G Q E F M I E K I N S A V C I P T D W V K V G S T K A V S R F H S P F I V E N Y R H L N Q L R E Q L V L D C S
A E W L D F L E K F S E H Y H S L C K A V H H L A T V D C I F S L A K V A K Q G D Y C R P T V Q E E R K I V I K N G R H P V D V L L G E Q D Q Y V P N N T D L S E D S E R V M
I I T G P N M G G K S S Y I K Q V A L I T I M A Q I G S Y V / P A E E A T I G I D G I F T R M G A A D N I Y K G R S T F M E E L T D A E I I R K A T S Q S L V I L D E L G R G T S T H
D G I A I A T A L E Y F I R D V K S L T L F V T H Y P P V C E L E K N Y S H Q V G N Y H M G F L V S E D E S K L D P G T A E Q V P D F V T F L Y Q I T R G I A R S Y G L N V A
K L A D V P G E I K K A H K S K E L E G L I N T K R K R L K Y F A K L W T M H I N A Q D L Q K W T E E F N M E E T Q T S L H

(-1)ORF (SEQ ID NO: 73)

MSRRKPASGGLAASSSAPARQAVLSRFFQSTGSLKSTSSSTGAADQVDPGAAAAAAAAAAPPAPPAPAFPPQLPPHVATEIDRR
KKRPLENDGPVKKVKKVQQKEGGSDLGMSGNSEPPKCLRTRNVSKSLEKLFECFCDSALPQSRVQTESLQERFAVLPKCTDFDDI
SLLHAKNAVSSEDSKRQINQKD TLF DLSQFGSSNTSHENLQKTASKSANKRSKSIYTPLELQYIEMKQQHKDAVLCECGYKYRFFG
E D A E I A A R E L N I Y C H L D H N F M T A S I P T H R L F V H V R R L V A K G Y K V G V V K Q T E A L K A I G D N R S S I F S R K L T A L Y T K S T L I G E D V N P L I K L D
D A V N V D E I M T D T S T S Y L L C I S E N K E N V R D K K R A T F L L A L W E C S L P Q A R L C L I V S R T L L V Q S

(+1)(-2)ORF (SEQ ID NO: 74)

MSRRKPASGGLAASSSAPARQAVLSRFFQSTGSLKSTSSSTGAADQVDPGAAAAAAAAAAPPAPPAPAFPPQLPPHVATEIDRR
KKRPLENDGPVKKVKKVQQKEGGSDLGMSGNSEPPKCLRTRNVSKSLEKLFECFCDSALPQSRVQTESLQERFAVLPKCTDFDDI
SLLHAKNAVSSEDSKRQINQKD TLF DLSQFGSSNTSHENLQKTASKSANKRSKSIYTPLELQYIEMKQQHKDAVLCECGYKYRFFG
E D A E I A A R E L N I Y C H L D H N F M T A S I P T H R L F V H V R R L V A K G Y K V G V V K Q T E A L K A I G D N R S S I F S R K L T A L Y T K S T L I G E D V N P L I K L D
D A V N V D E I M T D T S T S Y L L C I S E N K E N V R D K K (K) G Q H F Y W H C G S A A C H R R G C V

ACVR2,

(wt) ORF (SEQ ID NO: 107)

MGAAAKLAFA VFLISCSSGA ILGRSETQEC LFFNANWEKD RTNQTGVEPC YGDKDRRHC FATWKNISGS IEIVKQGCWL
DDINCYDRTD CVEKKDSPEV YFCCCEGNMC NEKFSYFPEM EVTQPTSNPV TPKPPYYNIL L YSLVPLMLI AGIVICAFWV

FIG. 2-7

YRHHK MAYPP VLVPTQDPGP PPPSPLLGLK PLQLLEVAKAR GRFGCVWKAQ LLNEYVAVKI FPIQDKQSWQ NEYEVYSLPG MKHENILQFI GAEKRGTSD VDLWLITAFH EKGSLSDLK ANVWSWNELC HIAETMARGL AYLHEDIPGL KDGHKPAISH RDIKSKNVLL KNNLTACIAD FGLALKFEAG KSAGDTHGQV GTRRYMAPEV LEGAINFQRD AFLRIDMYAM GLVLWELASR CTAADGPVDE YMLPFEETIG QHPSLEDMQE VVVKKKRKPV LRDYWQKHAG MAMLCETIEE CWDHDAEARL SAGCVGERIT QMQRLTNIIT DEDIVTV/VTM VTNVDPFPKE SSL*

A8, Pos. 451: -1 ORF (Mut.rate 16.3%) (SEQ ID NO: 108)

MGAAAKLAFA VFLISCSSGA ILGRSETQEC LFFNANWEKD RTNQTVGVEPC YGDKDKRRHC FATWKNISGS IEIVKQGCWL DDINCYDRD CVEKKTALKY IFVAVRAICV MKSFLIFRRW KSHSPLQIQL HLSHPITSC SIPWCHLC*

A8 Pos. 1476: -1 (Mut.rate 81.6%) (SEQ ID NO: 109)

MGAAAKLAFA VFLISCSSGA ILGRSETQEC LFFNANWEKD RTNQTVGVEPC YGDKDKRRHC FATWKNISGS IEIVKQGCWL DDINCYDRD CVEKKDSEPV YFCCCEGNMC NEKFSYFPEM EVTQPTSNPV TPKPPYYNL LYSLVPLMLI AGIVICAFVV YRHHK MAYPP VLVPTQDPGP PPPSPLLGLK PLQLLEVAKAR GRFGCVWKAQ LLNEYVAVKI FPIQDKQSWQ NEYEVYSLPG MKHENILQFI GAEKRGTSD VDLWLITAFH EKGSLSDLK ANVWSWNELC HIAETMARGL AYLHEDIPGL KDGHKPAISH RDIKSKNVLL KNNLTACIAD FGLALKFEAG KSAGDTHGQV GTRRYMAPEV LEGAINFQRD AFLRIDMYAM GLVLWELASR CTAADGPVDE YMLPFEETIG QHPSLEDMQE VVVKKKRGLF*

FLJ11053, A11 Pos. 1695, Mut.rate 52.2%

wt ORF (SEQ ID NO: 110)

MVLRKLSKKD VTTKLKAMQE FGTMCERDT ETVKGVLPYW PRIFCKISLD HDERRVREATQ QAFEKTLKV KKQLAPYLKS LMGYWLMACQ DTYPAAFAA KDAFEAAFFP SKQPEAIAFC KDEITSVLQD HLIKETPDTL SDPQTVPEEE REAKFYRVVT CSLLALKRLL CLLPDNELDS LEEKFKSLLS QNKFWKYGKH SVPQIRSAFY ELVSALCQRI PQLMKEEASK VSPSVLLSID DSDPIVCPAL WEAVLYTLTT IEDCWLVHVA KKSVPFKLST VIREGGRGLA TVIYPYLLPF ISKLPHSITN PKLDFFKNLF TSLVAGLSTE RTKTSSSESS AVISAFYECL RFIMQQNLGE EEEQMLVND QLIPFIDAVL KDPGLQHGQL FNHLAETLSS WEAKADTEKD EKTAHNLENV LIHFWERLSE ICVAKISEPE ADVESVLGV NLLQVLQKPK SSLKSSKKKN GKVRFADEI ESNKENEKCV SSEGEKIEGW ELTTEPSLTH NSSGLLSPKR KKPLEDLVCK LADISINYVN ERKSEQHLRF LSTLDSFSS SRVFKMILLGD EKQSIVQAKP LEIAKLVQKN PAVQFLYQKL IGWLNEQDRK DFGFLVDILY SALRCCDNDM

-1 ORF (SEQ ID NO: 111)

MVLRKLSKKD VTTKLKAMQE FGTMCERDT ETVKGVLPYW PRIFCKISLD HDERRVREATQ QAFEKTLKV KKQLAPYLKS LMGYWLMACQ DTYPAAFAA KDAFEAAFFP SKQPEAIAFC KDEITSVLQD HLIKETPDTL SDPQTVPEEE REAKFYRVVT CSLLALKRLL CLLPDNELDS LEEKFKSLLS QNKFWKYGKH SVPQIRSAFY ELVSALCQRI PQLMKEEASK VSPSVLLSID DSDPIVCPAL WEAVLYTLTT IEDCWLVHVA KKSVPFKLST VIREGGRGLA TVIYPYLLPF ISKLPHSITN PKLDFFKNLF TSLVAGLSTE RTKTSSSESS AVISAFYECL RFIMQQNLGE EEEQMLVND QLIPFIDAVL KDPGLQHGQL FNHLAETLSS WEAKADTEKD EKTAHNLENV LIHFWERLSE ICVAKISEPE ADVESVLGV NLLQVLQKPK SSLKSSKKK VRLDLMRYL KAIKRMKNVY LQKERRLKG N*

-2 ORF (SEQ ID NO: 112)

MVLRKLSKKD VTTKLKAMQE FGTMCERDT ETVKGVLPYW PRIFCKISLD HDERRVREATQ QAFEKTLKV KKQLAPYLKS LMGYWLMACQ DTYPAAFAA KDAFEAAFFP SKQPEAIAFC KDEITSVLQD HLIKETPDTL SDPQTVPEEE REAKFYRVVT CSLLALKRLL CLLPDNELDS LEEKFKSLLS QNKFWKYGKH SVPQIRSAFY ELVSALCQRI PQLMKEEASK VSPSVLLSID DSDPIVCPAL WEAVLYTLTT IEDCWLVHVA KKSVPFKLST VIREGGRGLA TVIYPYLLPF ISKLPHSITN PKLDFFKNLF TSLVAGLSTE RTKTSSSESS AVISAFYECL RFIMQQNLGE EEEQMLVND QLIPFIDAVL KDPGLQHGQL FNHLAETLSS WEAKADTEKD EKTAHNLENV LIHFWERLSE ICVAKISEPE ADVESVLGV NLLQVLQKPK SSLKSSKKK W*

+ 1 ORF (SEQ ID NO: 113)

MVLRKLSKKD VTTKLKAMQE FGTMCERDT ETVKGVLPYW PRIFCKISLD HDERRVREATQ QAFEKTLKV KKQLAPYLKS LMGYWLMACQ DTYPAAFAA KDAFEAAFFP SKQPEAIAFC KDEITSVLQD HLIKETPDTL SDPQTVPEEE REAKFYRVVT CSLLALKRLL CLLPDNELDS LEEKFKSLLS QNKFWKYGKH SVPQIRSAFY ELVSALCQRI PQLMKEEASK VSPSVLLSID DSDPIVCPAL WEAVLYTLTT IEDCWLVHVA KKSVPFKLST VIREGGRGLA TVIYPYLLPF ISKLPHSITN PKLDFFKNLF TSLVAGLSTE RTKTSSSESS AVISAFYECL RFIMQQNLGE EEEQMLVND QLIPFIDAVL KDPGLQHGQL FNHLAETLSS WEAKADTEKD EKTAHNLENV LIHFWERLSE ICVAKISEPE ADVESVLGV NLLQVLQKPK SSLKSSKKK W*

KIAA1052, A11 Pos. 689, Mut.rate 42.2%

wt ORF (SEQ ID NO: 114)

MAGRPLRIGD QLVLEEDYDE TYIPSEQEIL EFAREIGIDP IKEPELMWLA REGIVAPLPG EWKPCQDITG DIYYFNFANG QSMWDHPCDE HYRSLVIQER AKLSTSGAIK KKKKKKEKKD KKDRLDPKSS LALGSSLAPV HVPLGGLAPL RGLVDTPPSA LRGSQSVSLG SSVESGRQLG EMLPSQGLK TSAYTKGLL SIYEDKTALS LLGLGEETNE EDEEEESDNQS VHSSSEPLRN LHLDIGALGG DFYEESLRT SQPEEKKDVS LDSDAAGPPT PCKPSSPGAD SSLSSAVGKG RQGSGARPGL PEKEENEKSE PKICRNLVTP KADPTGSEPA KASEKEAPED TVDAGEEGSR REEAKEPKK KASALEEGSS DASQELEISE HMKEPQLSDS IASDPKSFGH LDFGFRSRIS EHLLDVDLS PVLGGCRQA QQPLGIEDKD DSQSSQDELQ SKQSGLEER YHRLSPPLPH EERAQSPPRS LATEEPPQG PEGQPEWKEA EELGEDSAAS LSLQLSLQRE QAPSPPAACE KGKEQHSQAE ELGPGQEEAE DPEEKVAVSP TPPVSPEVRS TEPVAPPEQL SEAALKAMEE AVAQVLEQDQ RHLLESQEK MQQLREKLCQ EEEEEEILRLH QQKEQSLSSL RERLQKAIEE EEARMREEES QRLSWLRAQV QSSTQADEDQ IRAEQEASLQ KLREELESQQ KAERASLEQK

FIG. 2-8

NRQMLEQLKE EIEASEKSEQ AALNAAKEKA LQQLREQLEG ERKEAVATLE KEHSAELERL CSSLEAKHRE VVSSLQKKIQ EAQQKEEAQL QKCLGQVEHR VHQKSYHVAQ YEHELSSLLR EKRQEVEGEH EERRLDKMKEE HQQVMAKARE QYEAEERKQR AELLGHLTGE LERLQRAHER ELETVRQEQQH KRLEDLRRRH REQERKLQDL ELDLETRAKD VKARLALLEV QEETARREKQ QLLDVQRQVA LKSEEATATH QQLEEAQKEH THLLQSNQQL REILDELQAR KLKLESQVQL LQAQSQQQLQK HFSSLEAEAQ KKQHLLREVT VEENNASPHF EPDLHIEDLR KSLGTNQTKE VSSSLSQSKE DLYLDSLSSH NVWHLLSAEG VALRSAKEFL VQQTRSMRRR QTALKAAQQH WRHELASAQE VAKDPPGIKA LEDMRKNLEK ETRHLDEMKS AMRKGHNLLK KKEEKLNLQLE SSLWEEASDE GTLGGSPTKK AVTFDLSMD SLSSESSESF SPPHLDSTPS LTSRKIHGLS HSLRQISSQL SSVLSILDSSL NPQSPPPPLA SMPAQLPPRD PKSTPTPTYY GSLARFSALS SATPTSTQWA WDSGQGPRLP SSVAQTVDDF LLEKWRKYFP SGIPLLSNSP TPLESRLGYM SASEQLRLLQ HSHSQVPEAG STTFQGIIEA NRRWLERVKN DPRPLFSST PKPKATLSLL QLGLDEHNRV KVYRF*

- 1 ORF (SEQ ID NO: 115)

MAGRPLRIGD QLVLEEDYDE TYIPSEQEIL EFAREIGIDP IKEPELMWLA REGIVAPLPG EWKPCQDITG DIYYFNFANG QSMWDHPCDE HYRSLVIQER AKLSTSGAIK KKKKKRKRKT RRTETPPKVR WPWPH*

- 2ORF (SEQ ID NO: 116)

MAGRPLRIGD QLVLEEDYDE TYIPSEQEIL EFAREIGIDP IKEPELMWLA REGIVAPLPG EWKPCQDITG DIYYFNFANG QSMWDHPCDE HYRSLVIQER AKLSTSGAIK KKKKKGKERQ EGQRPPQKF GLGFLISPSS CSSWGPGSFT RSCGYPTLCS SWISKREPG LSGVWTSAWR THAAFTGSQD DLCYKGSLGLH*

+ 1 ORF (SEQ ID NO: 117)

MAGRPLRIGD QLVLEEDYDE TYIPSEQEIL EFAREIGIDP IKEPELMWLA REGIVAPLPG EWKPCQDITG DIYYFNFANG QSMWDHPCDE HYRSLVIQER AKLSTSGAIK KKKKKGKER QEGQRPPQKF AGLGFLISP SCSSWGPGSF TRSCGYPTLCS SSWISKREPG ELSGVWTSAWR RTHAAFTGSQ DLCYKGSLG LH*